



Thu Jun 13 09:38:55 2002

us-09-743-194-4.rst

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2002, 10:08:05 ; Search time 1790.11 Seconds
(without alignments)
3769.868 Million cell updates/sec

Title: US-09-743-194-4
Perfect score: 500
Sequence: 1 ggaggctgcttcacgagcg.....taagtttatcatcatatcat 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estro: *
7: em_hcc: *
8: gb_est1: *
9: gb_est2: *
10: gb_hcc: *
11: gb_hcc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pin: *
16: em_gss_vit: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	405	81.0	470	12	AQ875364 V124P10 m
C 2	396.6	79.3	615	12	AQ502826 V74C11 mT
C 3	215	43.0	494	12	AQ875428 V125C3 mT
C 4	182.8	36.6	684	12	AQ502540 V116A mT
C 5	117	23.4	523	12	AQ875314 V122P2 mT
C 6	74.2	14.8	942	12	CNS00501
C 7	71	14.2	888	12	AZ549422 ENTBP49TF
C 8	70.2	14.0	833	12	CNS0082P
C 9	70.2	14.0	941	10	BM415213
C 10	69.6	13.9	570	12	CNS043EU
C 11	69.2	13.8	1110	12	CNS043EU
C 12	68.4	13.7	1046	12	CNS002KO
C 13	68.4	13.7	1135	12	CNS033GQ
C 14	68.2	13.6	1068	12	CNS002IV
C 15	67.8	13.6	1185	10	BF273407 GA_EB001
C 16	67.6	13.5	449	9	AL513999
C 17	67.2	13.4	694	12	AG044360 Pan trogl

18	67.2	13.4	1038	12	CNS0146B
19	67	13.4	638	12	AQ329262
C 20	67	13.4	1071	12	CNS00C6P
C 21	66.8	13.4	682	12	AG167085
C 22	66.6	13.3	431	12	CNS00YW2
C 23	66	13.2	898	12	CNS01812
C 24	66	13.2	1101	12	CNS01219
C 25	66	13.2	1101	12	CNS04XJP
C 26	65.6	13.1	859	12	AQ739567
C 27	65.6	13.1	1007	12	CNS06X9S
C 28	65.6	13.1	1885	10	BE420745
C 29	65.4	13.1	794	9	BE034370
C 30	65.4	13.1	930	10	BM415152
C 31	65.2	13.0	879	12	CNS00905
C 32	65	13.0	1101	12	CNS00RHB
C 33	64.8	13.0	425	9	AL514791
C 34	64.8	13.0	593	12	CNS00880
C 35	64.8	13.0	797	9	BE034282
C 36	64.8	13.0	870	12	AQ866797
C 37	64.8	13.0	1101	12	CNS00EXP
C 38	64.6	12.9	815	12	AQ853920
C 39	64.4	12.9	357	12	CNS0025V
C 40	64.4	12.9	712	12	AQ036635
C 41	64.4	12.9	713	9	BE041089
C 42	64.4	12.9	858	12	AZ199419
C 43	64.4	12.9	956	12	AQ330169
C 44	64.2	12.8	388	12	CNS011JK
C 45	64.2	12.8	764	12	AZ189318

ALIGNMENTS

RESULT 1	AQ875364/c	470 bp	DNA	linear	GSS 08-NOV-1999
LOCUS	V124E10 mTn-3XHA/lacZ Insertion Library, strain Y2278				Saccharomycetes
DEFINITION	cerevisiae genomic 5', DNA sequence.				
ACCESSION	AQ875364				
VERSION	AQ875364.1	GI:6287608			
KEYWORDS	SS.				
SOURCE	baker's yeast.				
ORGANISM	Saccharomycetes cerevisiae				
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
AUTHORS	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.				
TITLE	1 (bases 1 to 470)				
JOURNAL	Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,				
COMMENT	desBages, S.A., Cheung, K.H., Sheehan, A., Symonitis, D., Jansen, R.,				
	Umanak, L., Feldman, R., Nelson, K., Iwasaki, R., Kanada, D., Lugo, R.,				
	Hayes, J.L., Miller, R., Reder, G.S. and Snyder, M.				
	Genome Science Analysis of the Yeast Genome by Transposon Tagging and				
	Gene Disruption (1999)				
	Unpublished				
	Contact: Kumar A.				
	Michael Snyder, Dept. of Mol. Cell. and Dev. Biology				
	Yale University				
	P.O. Box 208103, New Haven, CT 06520-8103, USA				
	Tel: 203 432 9949				
	Fax: 203 432 6161				
	Email: anuj.kumar@yale.edu				
	Te of mTn-3XHA/lacZ insertion				
	Seq primer: GCGCTCTTCTTGGAGTAC				
	Class: transposon-tagged				
FEATURES	Location/Qualifiers				
Source	1..470				
	/organism="Saccharomycetes cerevisiae"				
	/strain="Y2278 - 5288C background, cir(0) rho(0)"				
	/db_xref="taxid:4932"				
	/clone_lib="mTn-3XHA/lacZ Insertion Library, strain Y2278"				
	/lab_host="E. coli"				
	/note="Vector: pHS56-Sal; A yeast genomic DNA library				
	without 2 micron or mitochondrial DNA was prepared in				
	pHS56-Sal; genomic DNA was size-fractionated (DNA of				

roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mtn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance.

```

BASE COUNT      188 a   99 c   96 g   87 t
ORIGIN

Query Match      81.0%; Score 405; DB 12; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 cgacgctcgggtgctcctacccatagatttcgctgctgcccacccacaaataagtaaacgtg 102
D 470 CGACGGTCCGGTGCCTATCCCTAGATTTTCGTCGCGCCGCCGACCAATAGTTAAAGCTG 411
QY 103 tggttatgggtgcacacagcgtttatcgtgttttatatcatgacgatgctgctccca 162
D 410 TGGTTATGGGTGCACACAGGCTTTATCGTGTGTTTATATCGATGCGGATTTGTGCCCTCCA 351
QY 163 gtgtattttgtatataccaaatgaagttctctacacaaattttatctttatcatcttagt 222
D 350 GTGTATTTTGTATATCAATTAAGGTTCTTACCTAACTTTATTTTATCACTTTAGT 291
QY 223 taatgctggttgcgtgtttctgctgtttctgtgctggttctctctctctctctctctct 282
D 290 TAACTGCTGTTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 231
QY 283 tctgtttccccccatgcgcgattggcgtttatggcgttatatatagacgaggttttta 342
D 230 TCGTGTGTCGCCCATCGCGATGGGCTTATATGCGTATATATAGCGAGGAGTTTAA 171
QY 343 cgtcgaagatcatctcagttgtgtgatagcctttctacttttacttttacttttcttctaac 402
D 170 CGTCGAAGATCATCTCAGTTGCTTGATAGCCCTTCTACTTTATTTACTTTCGTTTTTAA 111
QY 403 ctcatataacttagttttctgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 447
D 110 CTCATATATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 66

```

```

RESULT 2
ACCESSION A0502826/c
LOCUS V74C11 mtn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae
DEFINITION genomic 5', DNA sequence.
GSS 29-APR-1999

```

```

ACCESSION A0502826
VERSION A0502826.1 GI:4705372
KEYWORDS GSS.
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 616)
desEtages,S.A., Cheung,K.-H., Sheehan,A., Symoniatidis,D., Jansen,R.,
Umansky,L., Heidtman,M., Nelson,K., Iwasaki,H., Kanada,D., Lugo,R.,
Hager,K., Miller,P., Roeder,G.S. and Snyder,M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
Unpublished (1999)
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mtn-3xHA/lacZ insertion.
Seq primer: GGCTTCTTCTTGTGAAGTAC
Class: transposon-tagged
Location/Qualifiers
1. .616

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mtn-3xHA/lacZ insertion.
Seq primer: GGCTTCTTCTTGTGAAGTAC
Class: transposon-tagged
Location/Qualifiers
1. .616

```

```

FEATURES
source

```

```

/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/clone_lib="mtn-3xHA/lacZ Insertion Library"
/lab_host="E. coli"
/note="Vector: pHS56-Sal; A yeast genomic DNA library
(lacking mitochondrial DNA) was prepared in pHS56-Sal;
genomic DNA was size-fractionated (DNA of roughly 2-3 kb
in length) prior to cloning. This library was
subsequently mutagenized with a mtn-3xHA/lacZ
minitransposon containing lacZ, URA3, and tet resistance."
BASE COUNT      219 a   153 c   126 g   118 t
ORIGIN

```

```

Query Match      79.3%; Score 396.6; DB 12; Length 616;
Best Local Similarity 97.8%; Pred. No. 3.9e-56;
Matches 402; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ggaggtctgcttcacgagcgcggtgtgctgcttagttgcccacgacgctcgggtgctta 60
D 477 GGAAGTATGCTTCACGAGCGCGTGTGCGCATAGTATTGCCCGACGCTCCGGTGCTA 418
QY 61 tccctaattctctgctgccacccacaaatagtttaaacgctgctgttatggtgaccca 120
D 417 TCCATAGATTTTGTGTCGCCGCCGACCCATATAGCTTAAACGTCGTGTTATGGGTGCACCA 358
QY 121 gggcttattcgttttatatatcgatggcgattgtgctccagtgctatatttggatatcc 180
D 357 GGGCTTTATCGTGTGTTATATCGATGGCGATTTGTGCCCTCCAGTGATATTTTGTATATCC 298
QY 181 aattaaggtttcttacctaatttttttttatcatcttttagttaaagctggttgcctg 240
D 297 AATTAAGCTTCTTACCTAACTTTATTTTATCATCTTTAGTTAATGCTGTTGCTGCTG 238
QY 241 ttctgctgcttctctgctgcttctctctctctctctctctctctctctctctctctctct 300
D 237 TTCTGCTGCTTCTGCTGCGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
QY 301 ccgagggcttatagggcttatatatagacgaggttttaacgacgaagatactcag 360
D 177 CCGATGGGCTTATATGCGGTATATATATAGCGAGTGTTCAGTTCGTTTAACTCATATA 118
QY 361 ttgcttgatagccttctacttttacttttacttttctgcttttaacctcattata 411
D 117 TTTGCTTGATAGCTTCTACTTTATTTACTTTCTGTTTAACTCATATA 67

```

```

RESULT 3
ACCESSION A0875428/c
LOCUS A0875428
DEFINITION VI25C3 mtn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces
cerevisiae genomic 5', DNA sequence.
GSS 08-NOV-1999

```

```

ACCESSION A0875428
VERSION A0875428.1 GI:6287672
KEYWORDS GSS.
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 494)
Ross-Macdonald,P., Roemer,T., Coelho,P.S.R., Agarwal,S., Kumar,A.,
desEtages,S.A., Cheung,K.-H., Sheehan,A., Symoniatidis,D., Jansen,R.,
Umansky,L., Heidtman,M., Nelson,K., Iwasaki,H., Kanada,D., Lugo,R.,
Hager,K., Miller,P., Roeder,G.S. and Snyder,M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
Unpublished (1999)
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161

```

us-09-743-194-4.1st

Thu Jun 13 09:38:55 2002

Email: anuj.kumar@yale.edu
 Seq primer: GGCCTCTTCTTTGGAGATAC
 Class: transposon-tagged.

Location/Qualifiers
 1. 494
 /organism="Saccharomyces cerevisiae"
 /strain="Y2278 - S288C background, clr(0) rho(0)"
 /db_xref="taxon:4932"
 /clone_lib="mtn-3xHA/lacZ Insertion Library, strain Y2278"
 /lab_host="E. coli"
 /note="Vector: pHS56-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHS56-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mtn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance."

BASE COUNT 133 a 96 c 92 g 173 t

Query Match 43.0%; Score 215; DB 12; Length 494;
 Best Local Similarity 100.0%; Pred. No. 2.9e-26;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 tctgtgtcccccacgagtcgttatatggcgtatatatatagagcgagttttta 342
 DB 494 tctgtgtcccccacgagtcgttatatggcgtatatatatagagcgagttttta 435
 QY 343 cgtcgaagatcatctcagttgttgtagcccttctactttactttactttttaa 402
 DB 434 cgtcgaagatcatctcagttgttgtagcccttctactttactttactttttaa 375
 QY 403 ctcattatactttagtttcttctgagcgggtttttttctgtacttaaaagtccaa 462
 DB 374 ctcattatactttagtttcttctgagcgggtttttttctgtacttaaaagtccaa 315
 QY 463 caaagaacacatacaaaactacgtttatatcaatta 497
 DB 314 caaagaacacatacaaaactacgtttatatcaatta 280

RESULT 4
 AQ502540/c
 LOCUS
 DEFINITION V4164 mtn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', DNA sequence.
 ACCESSION AQ502540
 VERSION AQ502540.1 GI:4708190
 KEYWORDS GSS.
 SOURCE baker's yeast.
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE
 1 (bases 1 to 684)
 Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., DesEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatidis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
 Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
 Unpublished (1999)
 Contact: Kumar A
 Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
 Yale University
 P.O. Box 208103, New Haven, CT 06520-8103, USA
 Tel: 203 432 9949
 Fax: 203 432 6161
 Email: anuj.kumar@yale.edu
 te of mtn-3xHA/lacZ insertion.
 Seq primer: GGCCTCTTCTTTGGAGATAC
 Class: transposon-tagged.

FEATURES
 source
 Location/Qualifiers
 1. 684
 /organism="Saccharomyces cerevisiae"
 /db_xref="taxon:4932"
 /clone_lib="mtn-3xHA/lacZ Insertion Library"
 /lab_host="E. coli"
 /note="Vector: pHS56-Sal; A yeast genomic DNA library (lacking mitochondrial DNA) was prepared in pHS56-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mtn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance."

BASE COUNT 165 a 149 c 111 g 259 t

Query Match 36.6%; Score 182.8; DB 12; Length 684;
 Best Local Similarity 86.3%; Pred. No. 5e-21; 32; Indels 2; Gaps 1;
 Matches 214; Conservative 0; Mismatches 0;

QY 252 tctgtgcggttctctcct--ctctctgtgtttctgtgtgttcccccacgagtcgac 309
 DB 409 TTCTGTGCGGTTCCTAAATATATACAGATCATACAGTAATCCCCATCACCAGTGGAC 350
 QY 310 ttatatgctgtatatatatagagcgagttttacgtcgaagatcatctcagtttcttga 369
 DB 349 ATATATGCGGAAAATATATATAGAGCGAGATTTGACGTGGAAGATCATCTCAGTTTGTCTGA 290
 QY 370 tagccttctactttactttctgtttttaaactcattatacttagttttcttgatc 429
 DB 289 TAGCCTTTATATAAAATACTTTTCGTTAACTCATAAACTTTAGTTTATTTTGTATC 230
 QY 430 ggtttttctctatatactttaaagtccaatcaagaacacatacaaaactcgtttat 489
 DB 229 GGTTCCTTCCTGAATACCTTGAAGTTCAAAATCAAAAGGAACATACATAAACTACGTTTAT 170
 QY 490 atcaatta 497
 DB 169 ATCAATTA 162

RESULT 5
 AQ875314
 LOCUS
 DEFINITION V122F2 mtn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', DNA sequence.
 ACCESSION AQ875314
 VERSION AQ875314.1 GI:6287460
 KEYWORDS GSS.
 SOURCE baker's yeast.
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE
 1 (bases 1 to 523)
 Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., DesEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatidis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
 Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
 Unpublished (1999)
 Contact: Kumar A
 Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
 Yale University
 P.O. Box 208103, New Haven, CT 06520-8103, USA
 Tel: 203 432 9949
 Fax: 203 432 6161
 Email: anuj.kumar@yale.edu
 te of mtn-3xHA/lacZ insertion.
 Seq primer: GGCCTCTTCTTTGGAGATAC
 Class: transposon-tagged.

FEATURES
 source
 Location/Qualifiers
 1. 523

/clone_lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pHS1; Site 1: Bst I; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica
 using a method described by Clark and Diamond (Clark, a
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
 method for isolate identification. Exp. Parasitol.
 77:450.). The DNA was mechanically sheared to give a
 tight size distribution (~2 kb). The v-f-i method used for
 the library construction is described in detail in Smith,
 H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing. Projects in genome
 sequencing: A Practical Approach, eds. M. Vaudin and B.
 Borell, Oxford University Press, 1999)."
 BASE COUNT 582 a 62 c 40 g 204 t

Query Match 14.2%; Score 71; DB 12; Length 888;
 Best Local Similarity 49.3%; Pred. No. 0.011;
 Matches 185; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
 QY 125 ttatcgtgtttatcgcgagtgctgctccagtgatttttgatatacatt 184
 Db 822 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 763
 QY 185 aaggtcttaccatatttattttatcatttttgcgtggtgtgtgttc 244
 Db 762 GTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 703
 QY 245 tgcgtcttctgctgctcctctctctctctctctctctctctctct 304
 Db 702 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 643
 QY 305 tggcgttatggcgatataatagagcgagtttttcaagcgaatcctg 364
 Db 642 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 593
 QY 365 ctgtatagctttctacttacttctctctctctctctctctctctct 424
 Db 582 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 523
 QY 425 tgcgtggtttttctctgtatcactaaagtccaagcgaatcgaactacg 484
 Db 522 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 463
 QY 485 ttatatcaattaca 499
 462 AAAAAAATAAAAAA 448

RESULT 8
 CNS0082P/c 833 bp DNA linear GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
 DEFINITION BACR16P22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 ACCESSION AL051046
 VERSION AL051046.1 GI:4933192
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 833)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).

FEATURES
 source

1..833
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR16P22"
 /note="end : 77"

BASE COUNT 456 a 87 c 77 g 137 t 76 others
 ORIGIN

Query Match 14.0%; Score 70.2; DB 12; Length 833;
 Best Local Similarity 45.1%; Pred. No. 0.015; Indels 0; Gaps 0;
 Matches 153; Conservative 24; Mismatches 162;
 QY 113 gtgcaccaggcttgcgtgttttatatcgatggcgatttgccctccagtgatttt 172
 Db 387 GTGGCCATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 328
 QY 173 gtatatccaaataagggtttcttaacctaatatttttttttttttttttttt 232
 Db 327 TTTTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 268
 QY 233 ttgctctgttctgctgcttctctctctctctctctctctctctctctctct 292
 Db 267 TTTTAAATTTTGTGAAAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 208
 QY 293 ccccatcccgatggcggtatataatagcgagtttttcaagcgaat 352
 Db 207 KTAACGTTCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 148
 QY 353 catctcagtttgcgtatagccttctctctctctctctctctctctctctctac 412
 Db 147 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 88
 QY 413 tttagtttcttgatcggtttttttctctgtatactta 451
 Db 87 TTTGTTTTTTTATTTTWTGTTAATTAATTAATTAATTAATTAATTAATTA 49

RESULT 9
 BM415213 941 bp mRNA linear EST 28-JAN-2002
 LOCUS Op20285 Mixed Stage EST's from Globodera pallida, the potato cyst
 DEFINITION nematode Globodera pallida cDNA, mRNA sequence.
 ACCESSION BM415213
 VERSION BM415213.1 GI:18381667
 KEYWORDS EST.
 SOURCE Globodera pallida.
 ORGANISM Globodera pallida
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
 1 (bases 1 to 941)
 Heer, J., Sosinski, B., Pokrzywa, R.M., Warry, A. and Opperman, C.
 Mixed Stage EST's from Globodera pallida, the potato cyst nematode
 Unpublished (2001)
 Contact: Opperman, C
 Center for the Biology of Nematode Parasitism
 NC State University; IACR-Rothamsted
 Campus Box 7616; Raleigh, NC 27695, USA

	Query Match	13.6%	Score 67.8;	DB 10;	Length 1185;	
	Best Local Similarity	40.5%;	Pred. No. 0.032;			
	Matches 132;	Conservative	0;	Mismatches 194;	Indels	0; Gaps
Oy	125	tttatcgggttttatccgagtgctgcacaggatttggcttcagtatttttgtatcatccaatt	184			
Dd	577	TTTTTTTNNNTTT	636			
Oy	185	aagggttctaccctaattttatttttatcatcttttagttaatcggtgttgctcgtcttc	244			
Dd	637	NNTT	696			
Oy	245	tgcgtcttctgcgggttcctctctctctctctgttctcgtctcgtcctcccatacgca	304			
Dd	697	TTTTTTTNNNTNNNNNNNNNTNNTNNTNNTNNTNNTNNTNNTNNTNNTNNTWT	756			
Oy	305	tgggcttatcgcgctatatatagacgaggttttcaatcgagaatcatcgaatttg	364			
Dd	757	TNNNNNNNNNNNNNNNTTTTTNNTNNTNNTNNTNNTNNTNNTNNTTTTTTTT	816			
Oy	365	ctgatagaccttctactattactctcgttttttaacctaatatacttgaattctctt	424			
Dd	817	TT	876			
Oy	425	tgatcggtttttctctcgtatactt	450			
Dd	877	TTTTTTNNNTT	902			

search completed: June 12, 2002, 19:18:48
Job time: 33043 sec

